

**AMENDMENTS TO THE CLAIMS**

1-145. (Canceled)

146. (Previously amended) A functional cytochrome P450 oxygenase variant comprising a mutation of a glutamic acid residue at a position corresponding to amino acid 331 of cytochrome P450<sub>cam</sub> from *P. putida* (SEQ ID NO:2) and having at least 90% sequence identity to SEQ ID NO:2.

147. (Previously amended) The cytochrome P450 oxygenase variant of claim 146, wherein the mutant amino acid at the position corresponding to amino acid 331 is lysine.

148. (Previously amended) A functional cytochrome P450 oxygenase variant comprising at least one mutation of an arginine residue at a position corresponding to amino acid 280 of cytochrome P450<sub>cam</sub> from *P. putida* (SEQ ID NO:2) and having at least 90% sequence identity to SEQ ID NO:2.

149. (Previously amended) The cytochrome P450 oxygenase variant of claim 148, wherein the mutant amino acid at the position corresponding to amino acid 280 is leucine.

150. (Previously amended) A functional cytochrome P450 oxygenase variant comprising at least one mutation of a cysteine residue at a position corresponding to amino acid 242

of cytochrome P450<sub>cam</sub> from *P. putida* (SEQ ID NO:2) and having at least 90% sequence identity to SEQ ID NO:2.

151. (Previously amended) The cytochrome P450 oxygenase variant of claim 148, wherein the mutant amino acid at the position corresponding to amino acid 280 is phenylalanine.

152. (Currently amended) A functional cytochrome P450 oxygenase variant comprising at least one mutation at a position selected from the group consisting of amino acid positions 242, 280, and 331 of SEQ ID NO:2 and having at least 9099% sequence identity to SEQ ID NO:2.

153. (Previously amended) The cytochrome P450 oxygenase variant of claim 152 comprising at least one mutation selected from the group consisting of:

- (a) a glutamic acid to lysine mutation at position 331 of SEQ ID NO:2;
- (b) an arginine to leucine mutation at position 280 of SEQ ID NO:2; and
- (c) a cysteine to phenylalanine mutation at position 242 of SEQ ID NO:2.

154. (Previously amended) The variant cytochrome P450 oxygenase of claim 152, comprising at least one mutation selected from the group consisting of:

- (a) a glutamic acid to arginine or histidine mutation at position 331 of SEQ ID NO:2; and

(b) an arginine to isoleucine, methionine, or valine mutation at position 280 of SEQ ID NO:2.

155. Canceled.

156. (Currently amended) A cytochrome P450 oxygenase variant having a catalytic activity at least two times the catalytic activity of wild-type cytochrome P450<sub>cam</sub> oxygenase from *P. putida* (SEQ ID NO:2) in promoting the oxygenation of an oxygenase substrate in the presence of an oxygen donor, at least 9099% sequence identity to SEQ ID NO:2, and a mutation in at least one position corresponding to one of amino acids 242, 280, and 331 of SEQ ID NO:2.

157. (Previously amended) A cytochrome P450 oxygenase variant having a catalytic activity at least about ten times the catalytic activity of wild-type cytochrome P450<sub>cam</sub> oxygenase from *P. putida* (SEQ ID NO:2) in promoting the oxygenation of an oxygenase substrate in the presence of an oxygen donor, at least 90% sequence identity to SEQ ID NO:2, and a mutation in at least one position corresponding to one of amino acids 242, 280, and 331 of SEQ ID NO:2.

158. (Currently amended) A cytochrome P450 oxygenase variant having a stability at least two times the stability of wild-type cytochrome P450<sub>cam</sub> oxygenase from *P. putida* (SEQ ID NO:2) in promoting the oxygenation of an oxygenase substrate in the presence of an oxygen donor, at least 9099% sequence identity to SEQ ID NO:2, and a mutation in at least one position corresponding to one of amino acids 242, 280, and 331 of SEQ ID NO:2.

159. (Previously amended) A cytochrome P450 oxygenase variant having a stability at least about ten times the stability of wild-type cytochrome P450<sub>cam</sub> oxygenase from *P. putida* (SEQ ID NO:2) in promoting the oxygenation of an oxygenase substrate in the presence of an oxygen donor, at least 90% sequence identity to SEQ ID NO:2, and a mutation in at least one position corresponding to one of amino acids 242, 280, and 331 of SEQ ID NO:2.

160. (Allowed) A cytochrome P450 oxygenase variant comprising a sequence selected from the group consisting of SEQ ID NO:11, SEQ ID NO:12, and SEQ ID NO:13.

161. (Previously amended) An oxygenase variant evolved from a wild-type oxygenase enzyme, and having a catalytic activity at least ten times the catalytic activity of the wild-type oxygenase enzyme in promoting the oxygenation of an oxygenase substrate in the presence of an oxygen donor, which oxygenase variant was identified by a method comprising the steps of:

- (a) contacting a test enzyme variant with an oxygenase substrate and the oxygen donor under conditions allowing the formation of an oxygenated product if said test enzyme variant is an oxygenase enzyme;
- (b) providing a coupling enzyme which is capable of promoting the formation of a detectable composition from the oxygenated product;
- (c) detecting the detectable composition; and

(d) selecting any test enzyme having at least 10 times the catalytic activity of the wild-type oxygenase enzyme in the presence of the oxygen donor, at least 90% sequence identity to SEQ ID NO:2, and a mutation in at least one position corresponding to one of amino acids 242, 280, and 331 of SEQ ID NO:2.

162. (Pending) The oxygenase variant of claim 161, wherein the detecting of the detectable composition comprises detection of at least one of ultraviolet light, color change, fluorescence, and luminescence.

163. (Previously amended) The oxygenase variant of claim 161, wherein

(a) the organic substrate is selected from the group consisting of naphthalene, 3-phenylpropionate, benzene, toluene, benzoic acid, anthracene, benzphetamine, and coumarin;

(b) the oxygen donor is selected from the group consisting of hydrogen peroxide and t-butyl peroxide; and

(c) the coupling enzyme is selected from the group consisting of horseradish peroxidase, cytochrome c peroxidase, tulip peroxidase, lignin peroxidase, carrot peroxidase, peanut peroxidase, soybean peroxidase, and NOVOZYME® 502.

164. (Previously amended) An oxygenase variant evolved from a wild-type oxygenase enzyme, and having a stability at least ten times the stability of the wild-type oxygenase

enzyme in promoting the oxygenation of an oxygenase substrate in the presence of an oxygen donor, which oxygenase variant was identified by a method comprising the steps of:

- (a) contacting a test enzyme variant with an oxygenase substrate and the oxygen donor under conditions allowing the formation of an oxygenated product if said test enzyme variant is an oxygenase enzyme;
- (b) providing a coupling enzyme which is capable of promoting the formation of a detectable composition from the oxygenated product;
- (c) detecting the detectable composition; and
- (d) selecting any test enzyme having at least 10 times the stability of the wild-type oxygenase enzyme, at least 90% sequence identity to SEQ ID NO:2, and a mutation in at least one position corresponding to at least one of amino acids 242, 280, and 331 of SEQ ID NO:2.

165. (Pending) The oxygenase variant of claim 164, wherein the detecting of the detectable composition comprises detection of at least one of ultraviolet light, color change, fluorescence, and luminescence.

166. (Previously amended) The oxygenase variant of claim 164, wherein

- (a) the organic substrate is selected from the group consisting of naphthalene, 3-phenylpropionate, benzene, toluene, benzoic acid, anthracene, benzphetamine, and coumarin;
- (b) the oxygen donor is selected from the group consisting of hydrogen peroxide and t-butyl peroxide; and

(c) the coupling enzyme is selected from the group consisting of horseradish peroxidase, cytochrome c peroxidase, tulip peroxidase, lignin peroxidase, carrot peroxidase, peanut peroxidase, soybean peroxidase, and NOVOZYME® 502.

167. (Currently amended) A functional cytochrome P450 oxygenase variant identified by a method comprising the steps of:

- (a) contacting a test cytochrome P450 oxygenase variant with an oxygenase substrate and an oxygen donor under conditions allowing the formation of an oxygenated product if said test enzyme variant is an oxygenase enzyme;
- (b) providing a coupling enzyme which is capable of promoting the formation of a detectable composition from the oxygenated product;
- (c) detecting the detectable composition; and
- (d) selecting any test enzyme having a mutation at a position corresponding to at least one of amino acid 331, 280, and 242 of cytochrome P450<sub>cam</sub> from *P. putida* (SEQ ID NO:2) and at least 9099% sequence identity to SEQ ID NO:2.

168. (Previously added) The cytochrome P450 oxygenase variant of claim 167, wherein the detecting of the detectable composition comprises detection of at least one of ultraviolet light, color change, fluorescence, and luminescence.

169. (Previously amended) The cytochrome P450 oxygenase variant of claim 167, wherein

(a) the organic substrate is selected from the group consisting of naphthalene, 3-phenylpropionate, benzene, toluene, benzoic acid, anthracene, benzphetamine, and coumarin;

(b) the oxygen donor is selected from the group consisting of hydrogen peroxide and t-butyl peroxide; and

(c) the coupling enzyme is selected from the group consisting of horseradish peroxidase, cytochrome c peroxidase, tulip peroxidase, lignin peroxidase, carrot peroxidase, peanut peroxidase, soybean peroxidase, and NOVOZYME® 502.

170. (Previously added) The cytochrome P450 variant of claim 146, comprising a mutation at amino acid 331 of SEQ ID NO:2.

171. (Previously added) The cytochrome P450 variant of claim 148, comprising a mutation at amino acid 280 of SEQ ID NO:2.

172. (Previously added) The cytochrome P450 variant of claim 150, comprising a mutation at amino acid 242 of SEQ ID NO:2.

173. (Previously added) The cytochrome P450 variant of claim 152, comprising mutations at amino acids 242, 280, and 331 of SEQ ID NO:2.

174. (Canceled)

175. (Previously amended) The cytochrome P450 variant of claim 156, comprising at least one mutation selected from lysine at amino acid 331, leucine at amino acid 280, and phenylalanine at amino acid 242.

176. (Previously added) The cytochrome P450 variant of claim 156, wherein the oxygen donor is a peroxide.

177. (Previously added) The cytochrome P450 variant of claim 176, wherein the peroxide is selected from hydrogen peroxide and t-butyl peroxide.

178. (Canceled)

179. (Previously amended) The cytochrome P450 variant of claim 157, comprising at least one mutation selected from lysine at amino acid 331, leucine at amino acid 280, and phenylalanine at amino acid 242.

180. (Previously added) The cytochrome P450 variant of claim 157, wherein the oxygen donor is a peroxide.

181. (Previously added) The cytochrome P450 variant of claim 180, wherein the peroxide is selected from hydrogen peroxide and t-butyl peroxide.

182. (Canceled)

183. (Previously amended) The cytochrome P450 variant of claim 158, comprising at least one mutation selected from lysine at amino acid 331, leucine at amino acid 280, and phenylalanine at amino acid 242.

184. (Previously added) The cytochrome P450 variant of claim 158, wherein the oxygen donor is a peroxide.

185. (Previously added) The cytochrome P450 variant of claim 184, wherein the peroxide is selected from hydrogen peroxide and t-butyl peroxide.

186. (Canceled)

187. (Previously amended) The cytochrome P450 variant of claim 159, comprising at least one mutation selected from lysine at amino acid 331, leucine at amino acid 280, and phenylalanine at amino acid 242.

188. (Previously added) The cytochrome P450 variant of claim 159, wherein the oxygen donor is a peroxide.

189. (Previously added) The cytochrome P450 variant of claim 184, wherein the peroxide is selected from hydrogen peroxide and t butyl peroxide.